Fig. 1.

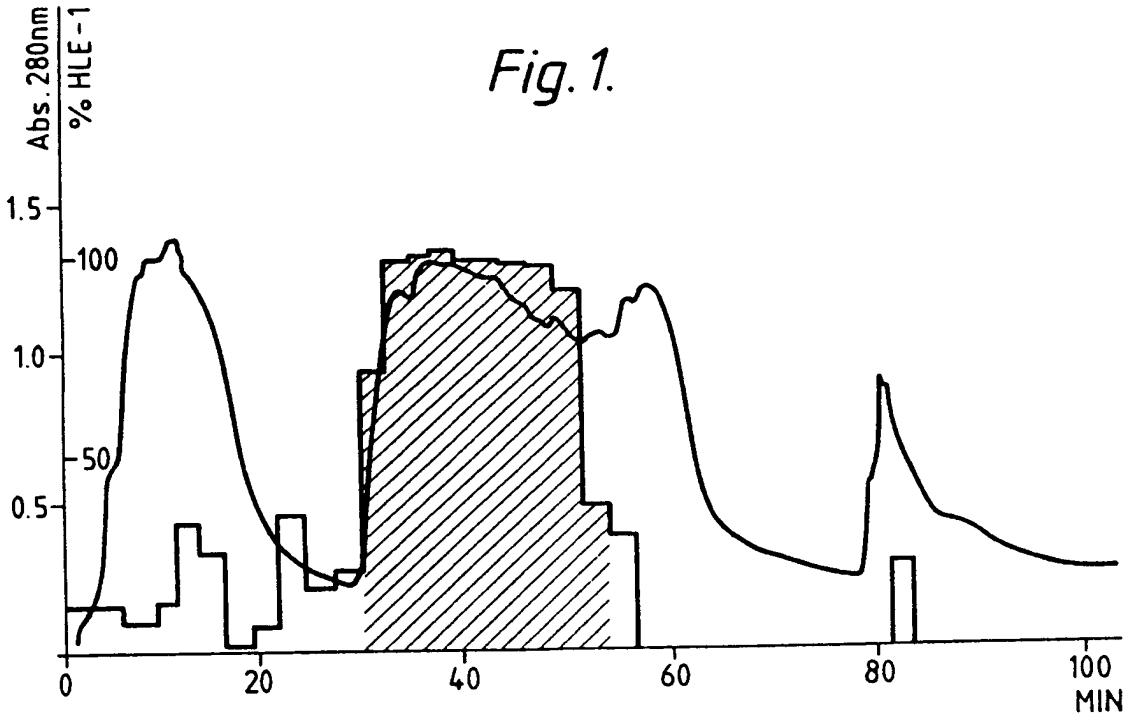


Fig. 2.

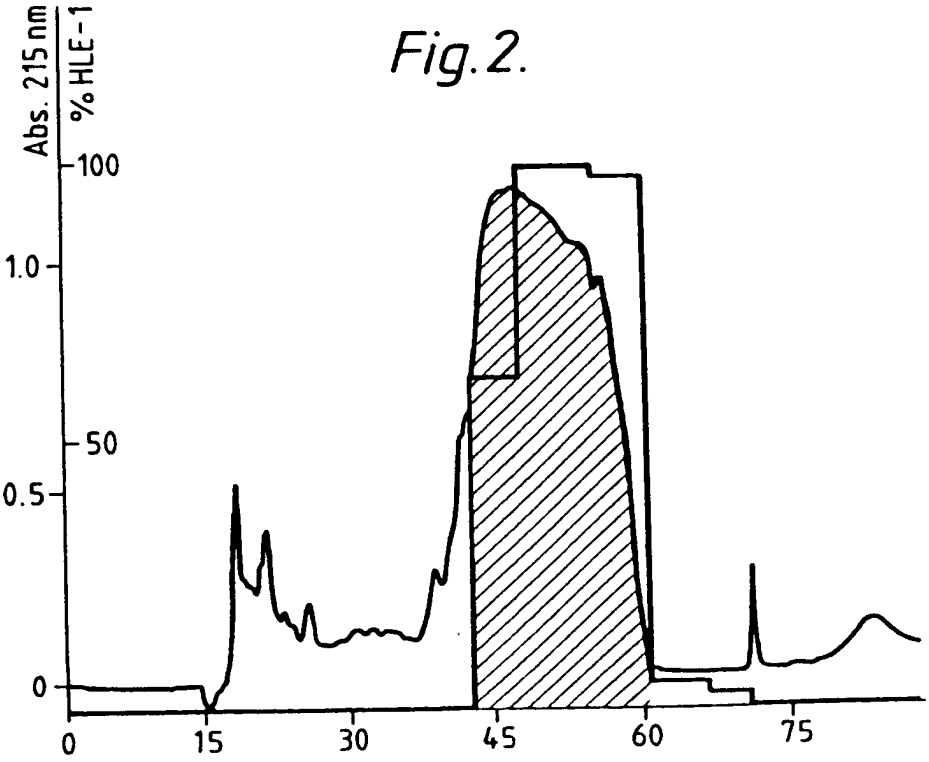


Fig.3.

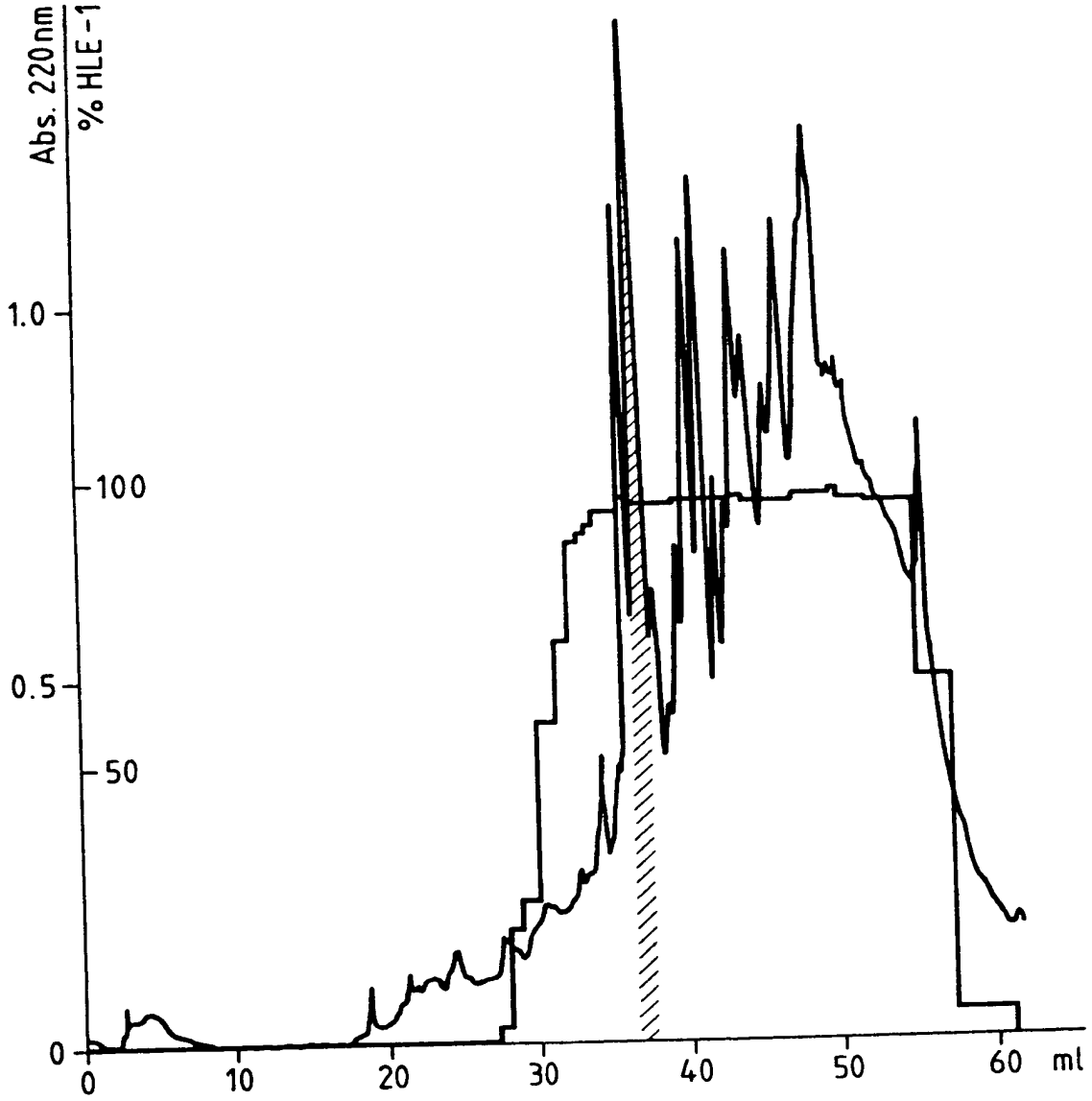


Fig. 4.

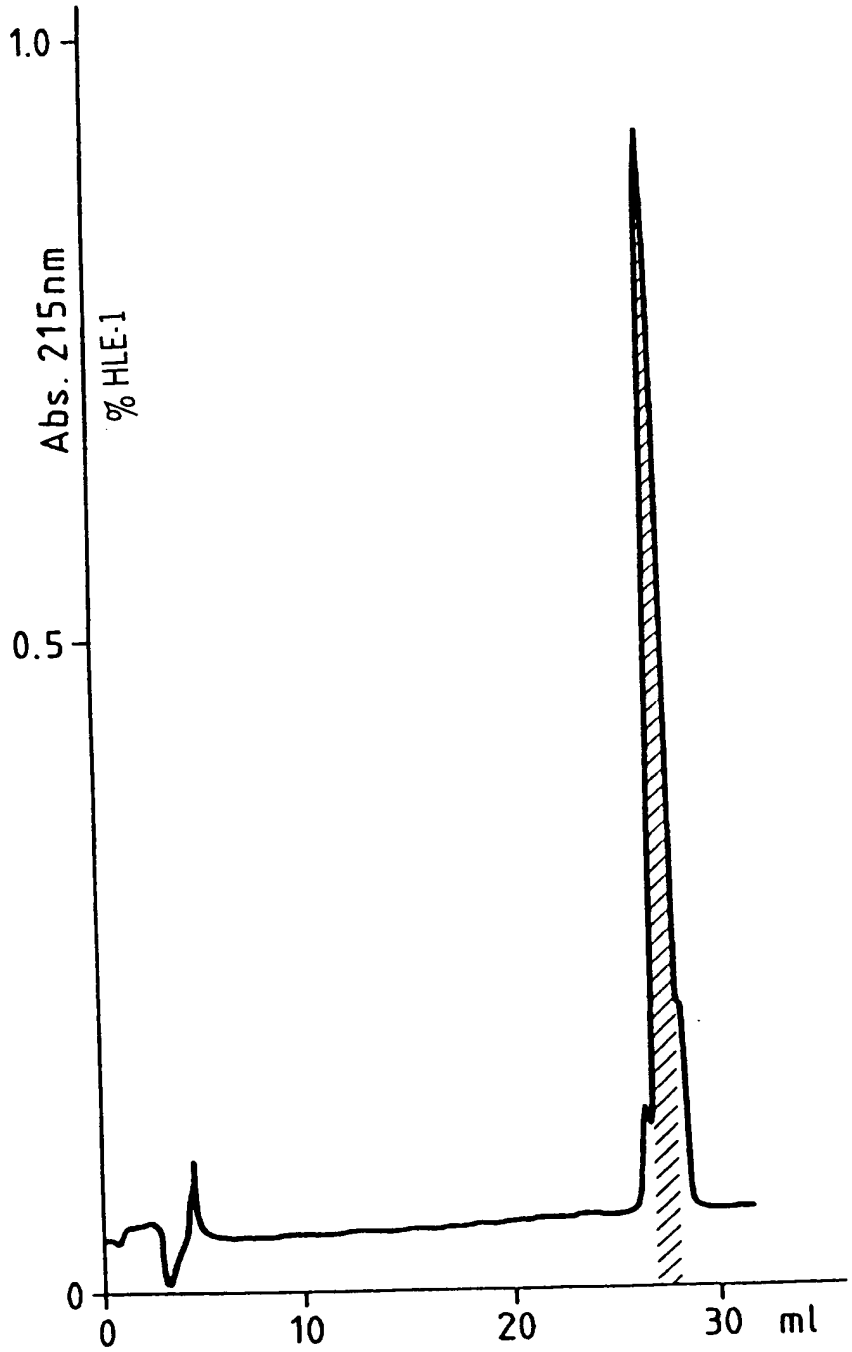


Fig. 5.

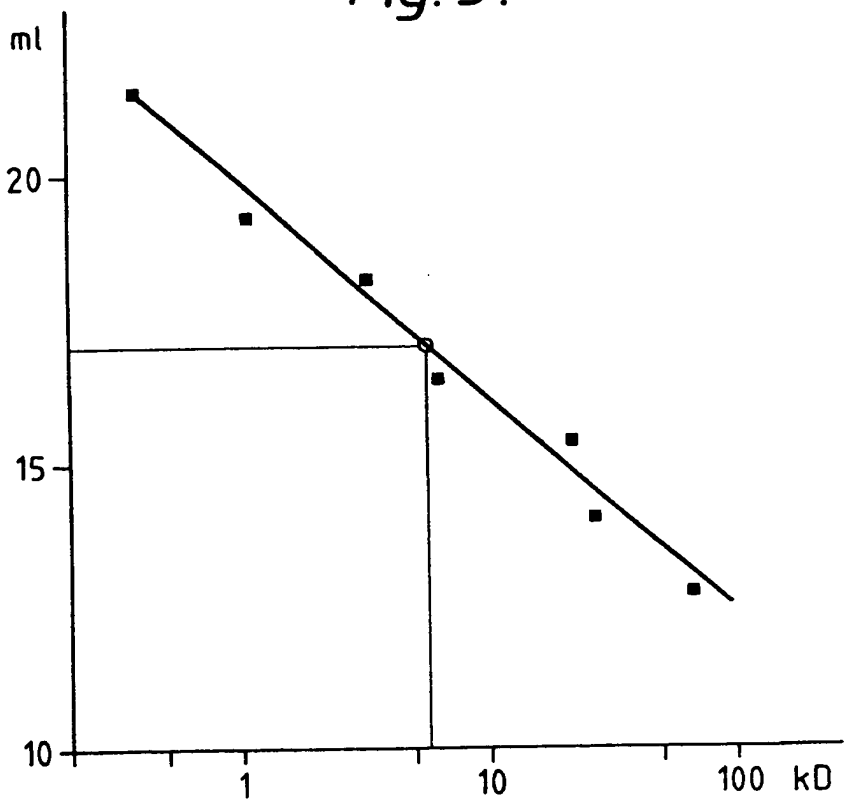


Fig. 7.

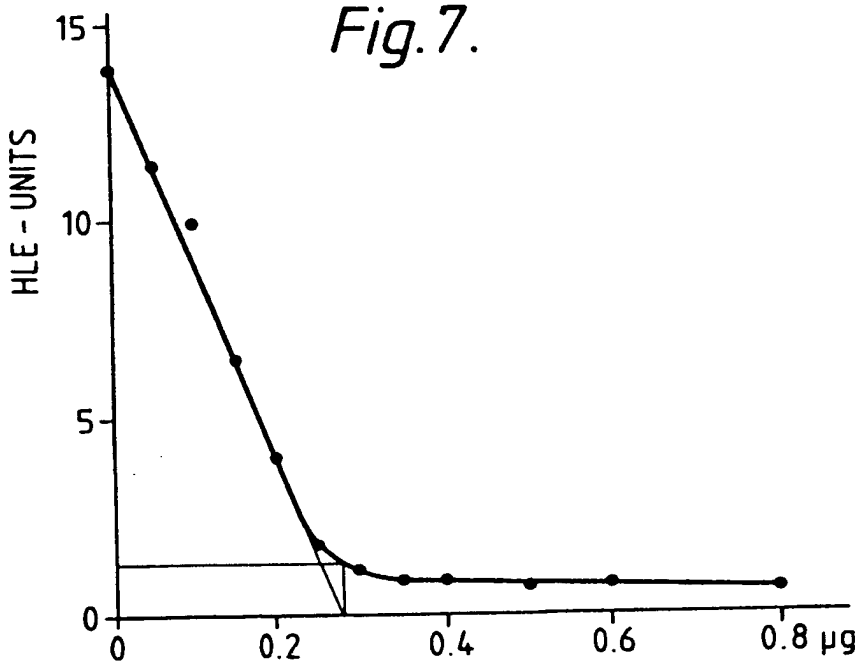
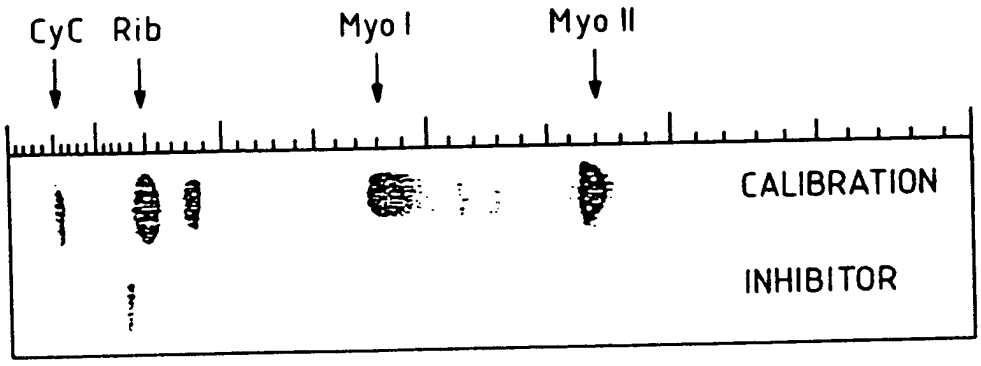


Fig.6.


CyC
Rib
Myo I
Myo II
CALIBRATION
INHIBITOR

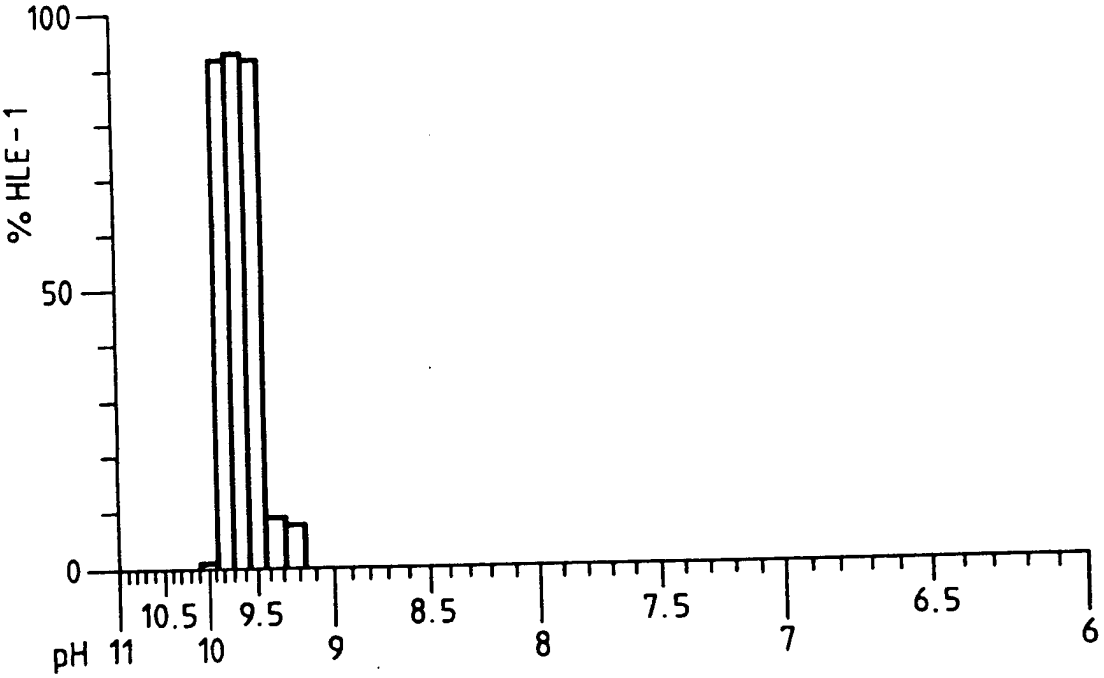

100
50
0
% HLE-1
pH 11
10.5
10
9.5
9
8.5
8
7.5
7
6.5
6

Fig.8.

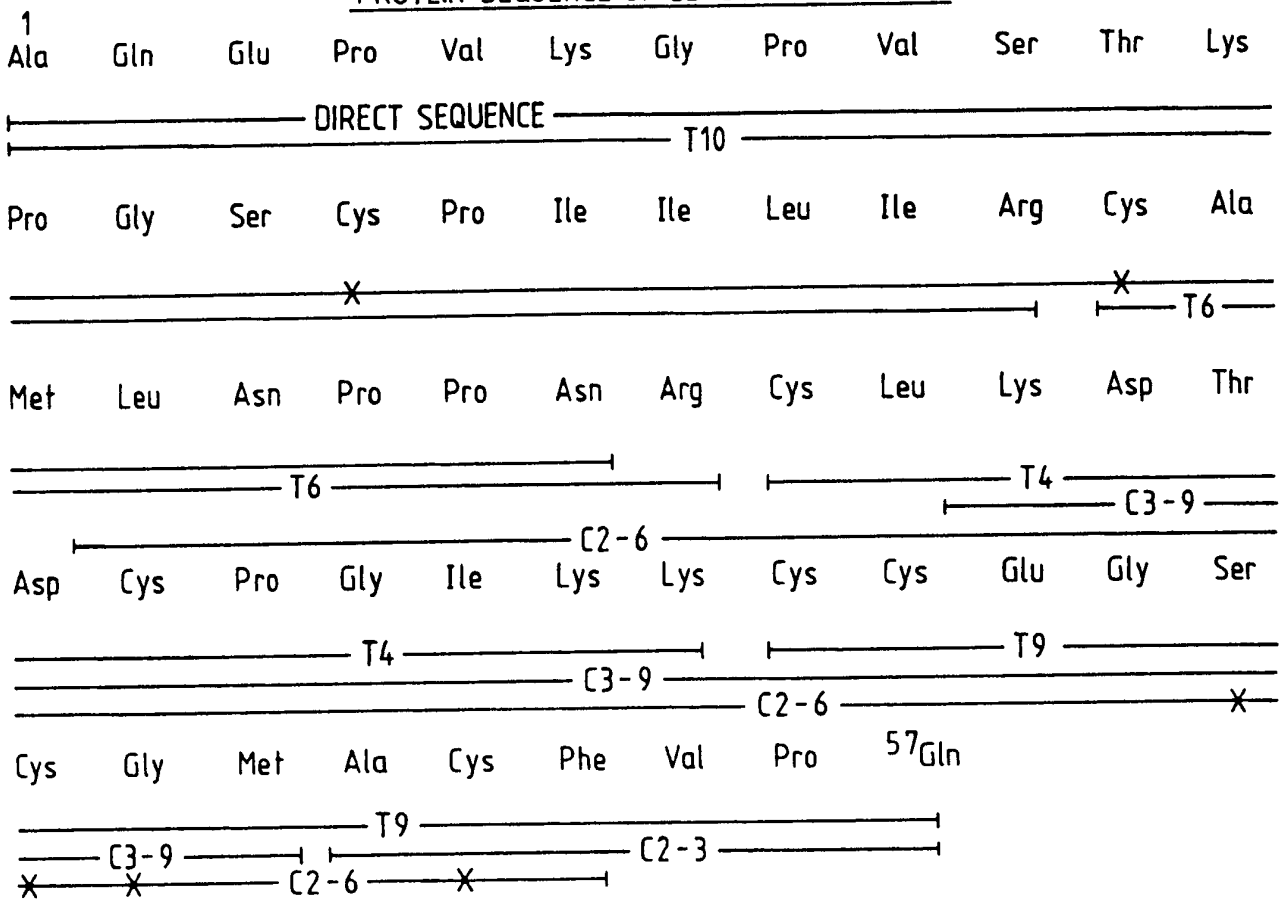


Fig. 9.

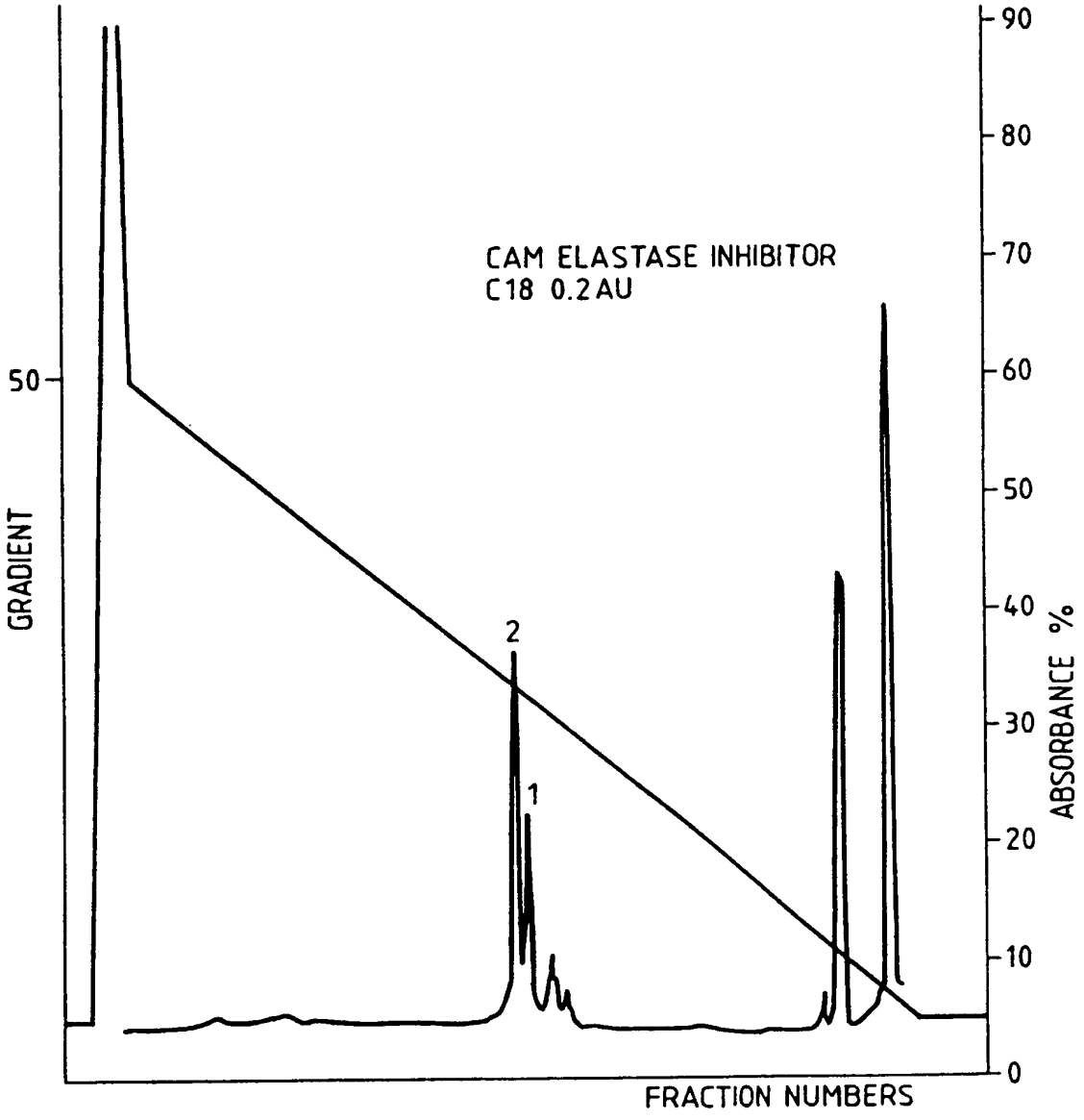

CAM ELASTASE INHIBITOR
C18 0.2AU
GRADIENT
50
ABSORBANCE %
90
80
70
60
50
40
30
20
10
0
1
2
FRACTION NUMBERS

Fig.10.

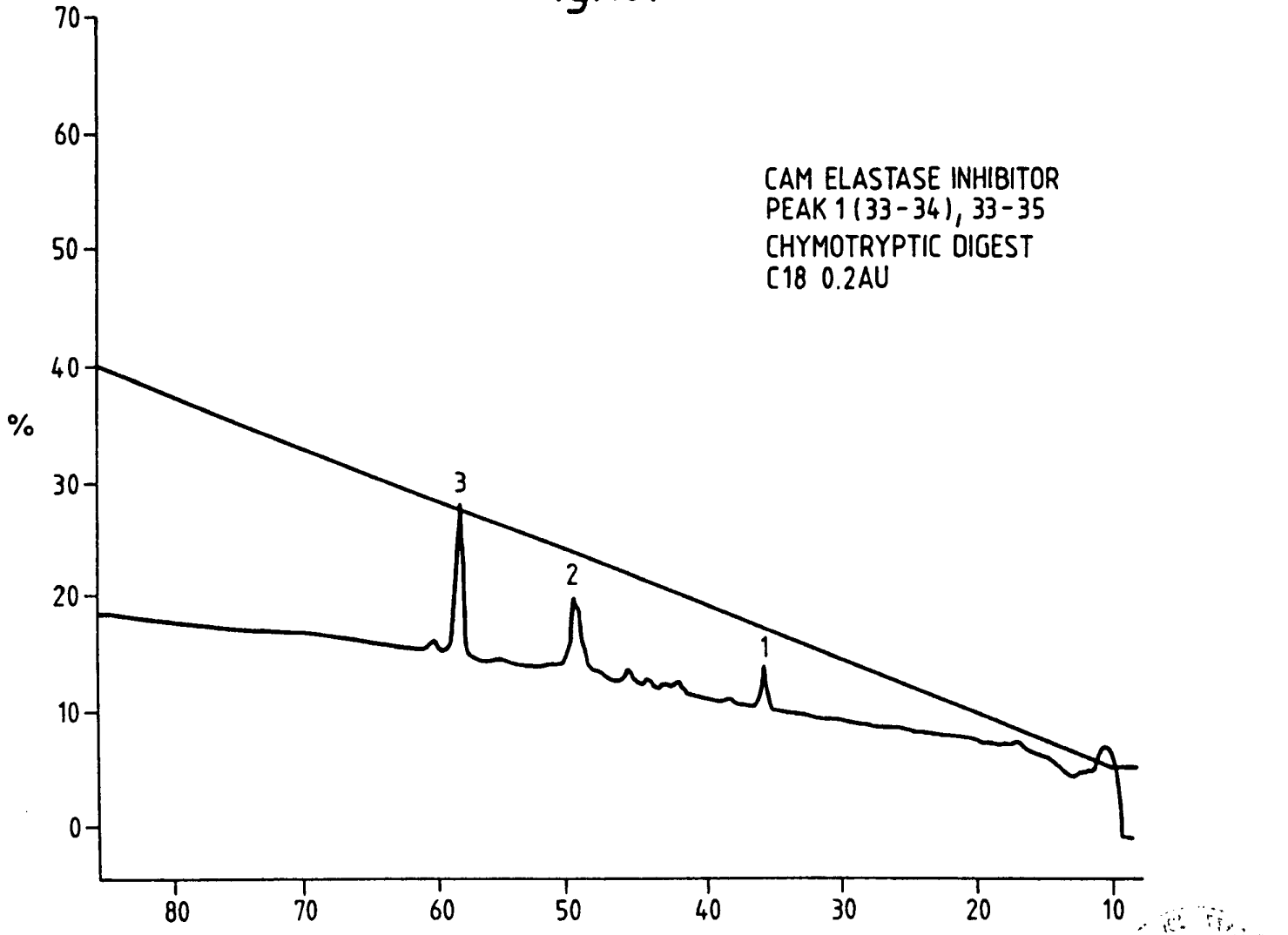


Fig. 11.

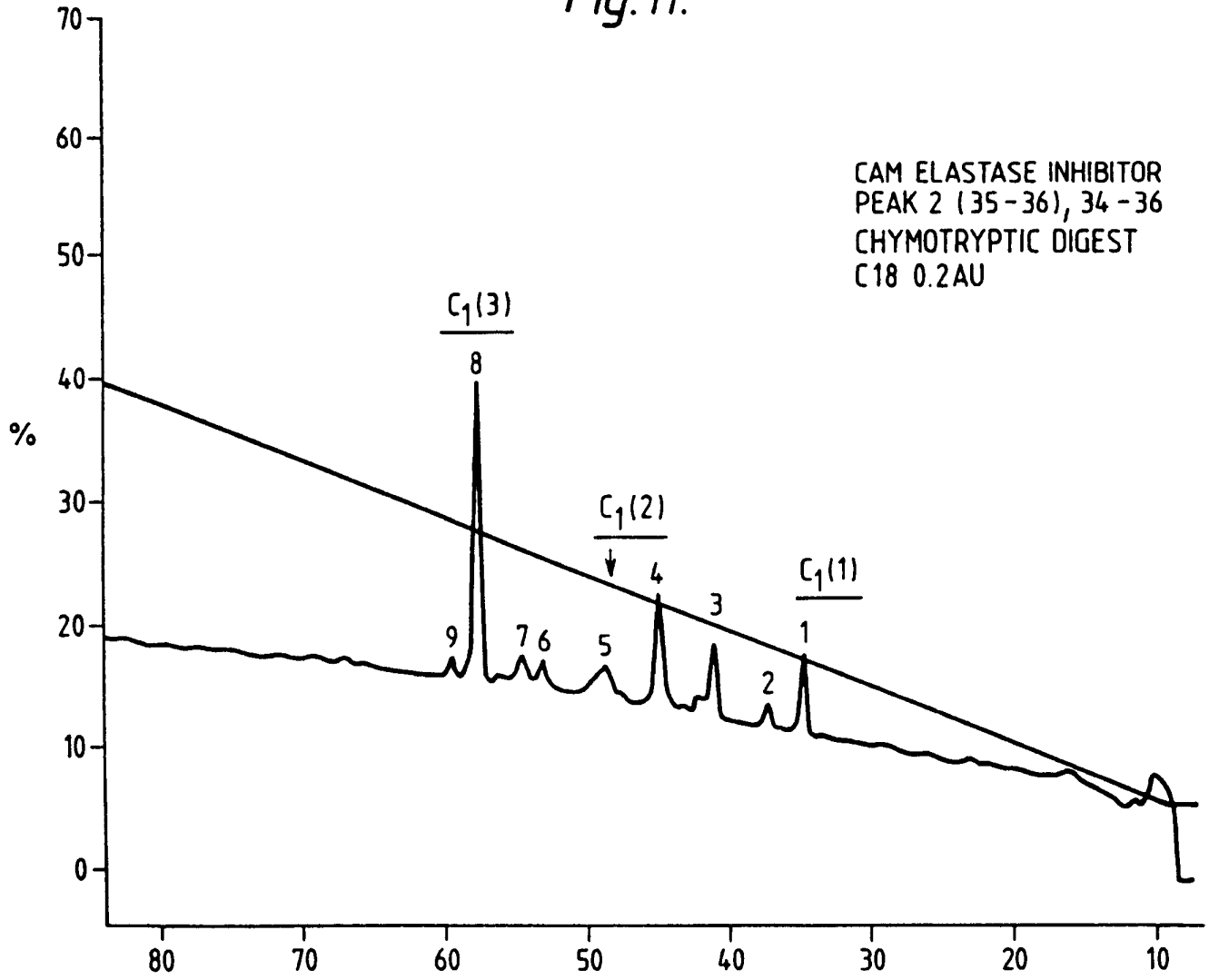


Fig. 12.

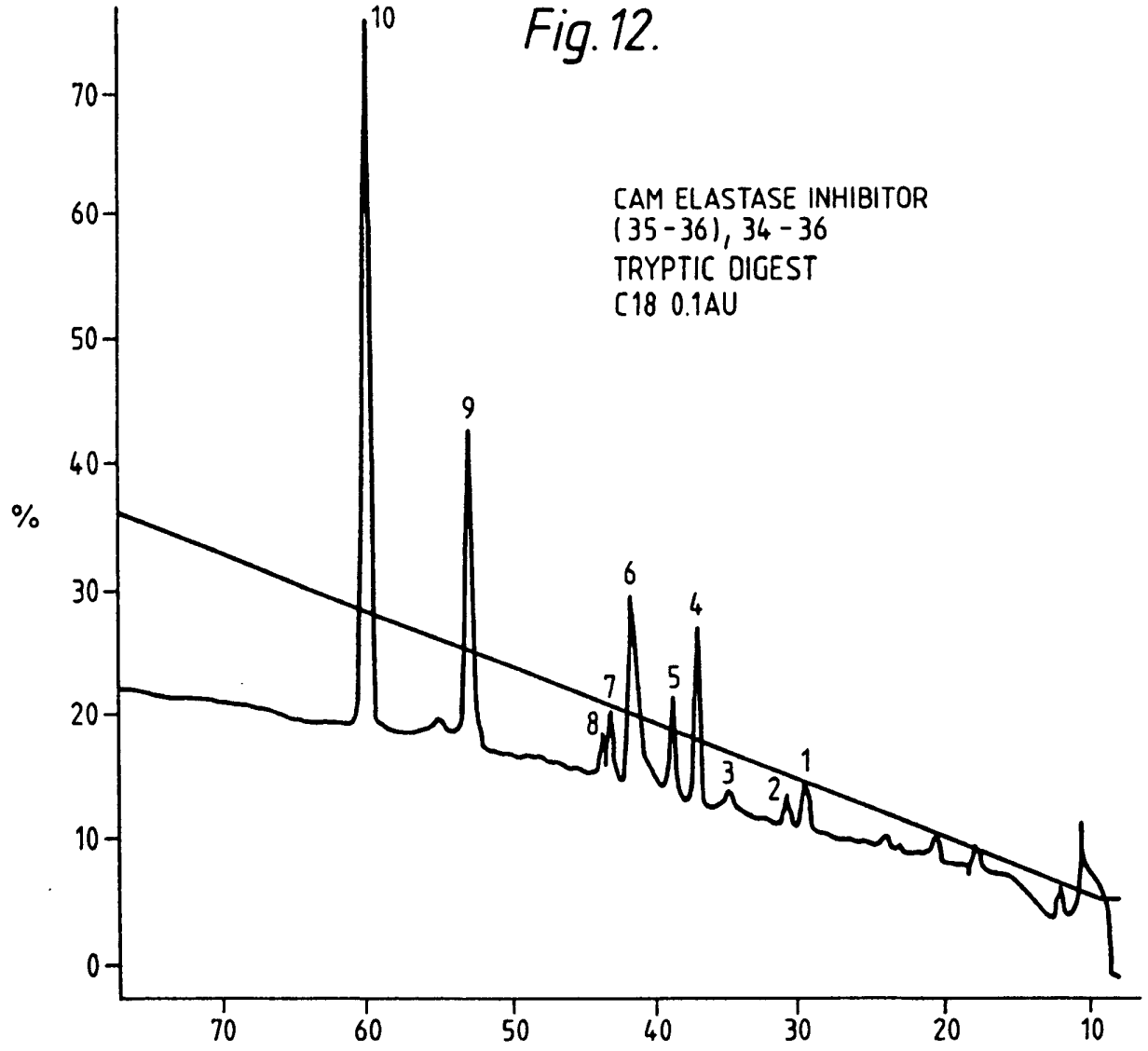


Fig. 13.

Fig. 14.

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys

GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC

5′ DNA

Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys

CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln

TGC GGG ATG GCC TGT TTC GTT CCC CAG

Z = T, C or A

P = A or G

Fig. 19.

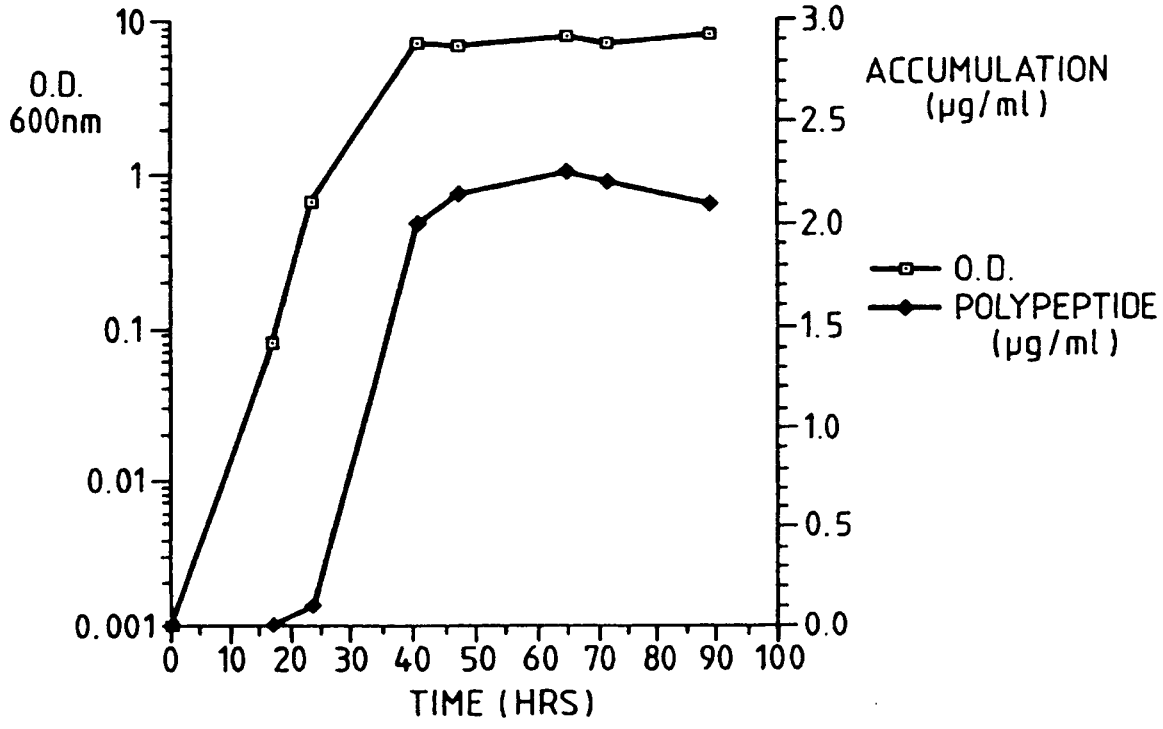


Fig. 15.

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC
5' DNA
Sequence

Pro Ile Ile Leu Ile Arg Cys Ala Met Leu Asn Pro Pro Asn Arg Cys
CCC ATT ATC TTG ATC CGG TGC GCC ATG TTG AAT CCC CCT AAC CGC TGC

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

TTG AAA GAT ACT GAC TGC CCA GGA ATZ AAG AAP TGC TGT GAA GGC TCT

Cys Gly Met Ala Cys Phe Val Pro Gln
TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

GCCGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCACACTGTCCA
TTCTTCCTCCCATTCAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACTTTCCAATAAAGAGTTCCG
GAATTC

Poly A 3'
signal

Z = T, C or A
P = A or G

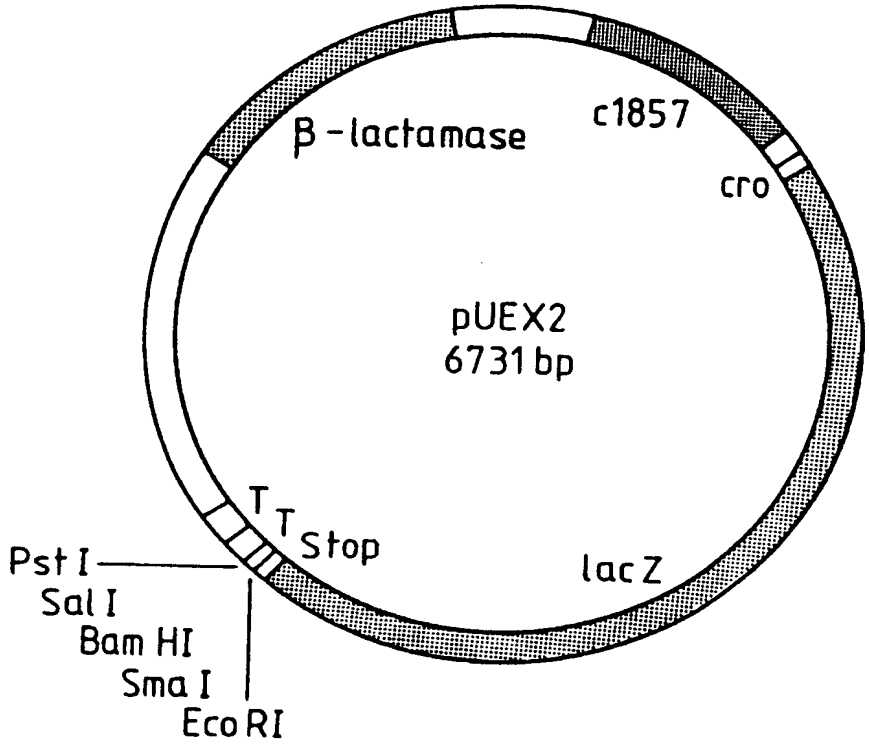
Fig. 16.

```
                    10                  30                  50
.         .         .         .         .         .
GGAATTCCGGTTCCTCATCGCTGGGACGCTGGTTCTAGAGGCAGCTGTCACGGGAGTTCC
EcoRI                                 XbaI
F  L  I  A  G  T  L  V  L  E  A  A  V  T  G  V  P
|-------IN-FRAME UPSTREAM PROTEIN SEQUENCE------
70                  90                  110
.         .         .         .         .         .
TGTTAAAGGTCAAGACACTGTCAAAGGCCGTGTTCCATTCAATGGACAAGATCCCGTTAA
V  K  G  Q  D  T  V  K  G  R  V  P  F  N  G  Q  D  P  V  K
130                 150                 170
.         .         .         .         .         .
AGGACAAGTTTCAGTTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCC
G  Q  V  S  V  K  G  Q  D  K  V  K
AlaGlnGluProValLysGlyPr
|--ELASTASE INHIBITOR--
```

Fig. 16 (cont.)

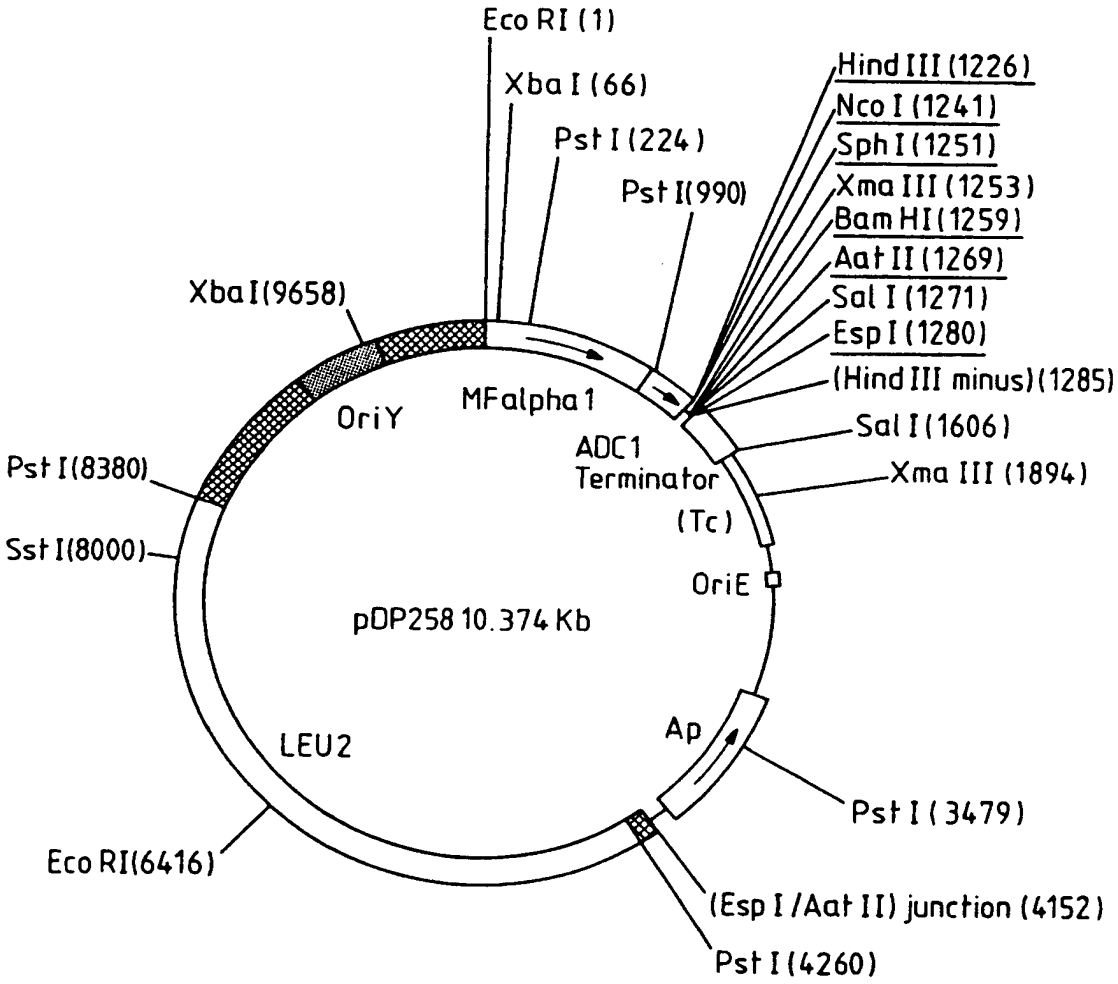
```
          190                 210                 230
           .         .         .         .         .         .
AGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTGATCCGGTGCGCCATGTTGAATCC
oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

          250                 270                 290
           .         .         .         .         .         .
CCCTAACCGCTGCTTGAAAGATACTGACTGCCCAGGAATCAAGAAGTGCTGTGAAGGCTC
oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe
          310                 330                 350
           .         .         .         .         .         .
TTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAGGGAGCCGGTCCTTGCTGCACCTGTGC
rCysGlyMetAlaCysPheValProGlnEnd
          370                 390                 410
           .         .         .         .         .         .
CGTCCCCAGAGCTACAGGCCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCAC

          430                 450                 470
           .         .         .         .         .         .
ACTGTCCATTCTTCCTCCCATTCAGGATGCCCACGGCTGGAGCTGCCTCTCTCATCCACT

          490
           .         .
TTCCAATAAAGAGTTCCGGAATTC
     Poly A          EcoRI
     signal
```

Fig. 17.




```
          EcoRI  SmaI BamHI   SalI          PstI
          |      |    |      |             |
pUEX2     GAA TTC CCG GGG ATC CGT CGA CCT GCA GCC AAG CTT GCT GAT TGA
          Glu Phe Pro Gly Ile Arg Arg Pro Ala Ala Lys Leu Ala Asp ***
```

Fig. 18.


Eco RI (1)
Xba I (66)
Pst I (224)
Pst I(990)
Hind III (1226)
Nco I (1241)
Sph I (1251)
Xma III (1253)
Bam HI (1259)
Aat II (1269)
Sal I (1271)
Esp I (1280)
(Hind III minus) (1285)
Sal I (1606)
Xma III (1894)
Xba I(9658)
OriY
MFalpha 1
ADC1
Terminator
(Tc)
Pst I(8380)
Sst I(8000)
OriE
pDP258 10.374 Kb
Ap
LEU2
Pst I (3479)
Eco RI(6416)
(Esp I /Aat II) junction (4152)
Pst I (4260)